

From: Chan, Christina
Sent: Wednesday, July 27, 2005 4:01 PM
To: Basi, Nirmal; STIC-Biotech/ChemLib
Subject: RE: Rush search for App. # 10/016,496

Please rush. Thanks Chris

Chris Chan
SPE, 1644
TC 1600 New Hire Training Coordinator
571-272-0841
Remsen 3E89

-----Original Message-----

From: Basi, Nirmal
Sent: Wednesday, July 27, 2005 3:59 PM
To: Chan, Christina
Subject: Rush search for App. # 10/016,496

Christina I am seeking approval for a RUSH sequence search, as indicated below. If approved, could you please forward the search to STIC and cc a copy to me.

Examiner: Nirmal S. Basi
Art Unit 1646
Office: Remsen Building, Room 4D68
Mail Room: Remsen Building, room 4C70

Sequence search:

App. #: 10/016,496
Result format: Paper.

Title: POLYCATION-SENSING RECEPTOR IN AQUATIC SPECIES AND METHODS
OF USE THEREOF

Inventors: William Harris et al

Priority Date: 3/27/96
Please search:
i) SEQ ID NOS: 1 and 2

Search issued, commercial databases and pending databases.

Thanks,
Nirmal S. Basi

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: 7/27/05
Date Completed: 8/1/05
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: 1 AA#: 1
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: QDA
WWW/Internet: _____
Other(Specify): _____

RESULT 2
 CDSR HUMAN
 STANDARD, PRT, 1078 AA.
 01-FEB-1995 (Rel. 31, Created)
 01-NOV-1995 (Rel. 32, Last sequence update)
 01-OCT-2004 (Rel. 45, Last annotation update)

DE Extracellular calcium-sensing receptor precursor (CAsR) (Parathyroid
 Cell calcium-sensing receptor).
 GN Name=CAsR; Synonyms=GPRC2A, PCAR1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pearce S.H.S., Thakker R.V.,
 RL Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Parathyroid;
 RX MEDLINE=95279439; PubMed=7759551; DOI=10.1074/jbc.270.21.12919;
 RA Garrett J.B., Capuano I.V., Hammerland L.G., Hung B.C., Brown B.M.,
 RA Hebert S.C., Nemeth B.F., Fuller P.,
 RT "Molecular cloning and functional expression of human parathyroid
 RT calcium receptor cDNAs.",
 RL J. Biol. Chem. 270:12919-12925 (1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=95408281; PubMed=7677761;
 RA Alda K., Kolsh S., Tawata M., Onaya T.,
 RT "Molecular cloning of a putative Ca(2+)-sensing receptor cDNA from
 RT human kidney.",
 RL Biochem. Biophys. Res. Commun. 214:524-529 (1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96343809; PubMed=8756555; DOI=10.1210/en.137.9.3842;
 RA Freichel M., Zink-Lorenz A., Holltsch A., Hafner M., Plockert V.,
 RA Raue F.,
 RT "Expression of a calcium-sensing receptor in a human medullary thyroid
 RT carcinoma cell line and its contribution to calcitonin secretion.",
 RL Endocrinology 137:3842-3848 (1996).
 RN [5]
 RP SEQUENCE OF 643-908 FROM N.A.
 RX MEDLINE=96133893; PubMed=8613532;
 RA Bixle D.D., Ratnam A., Mauro T., Harrie J., Pillai S.,
 RT "Changes in calcium responsiveness and handling during keratinocyte
 RT differentiation. Potential role of the calcium receptor.",
 RL J. Clin. Invest. 97:1085-1093 (1996).
 RN [6]
 RP VARIANTS FHH GLN-185, LYS-297 AND TRP-795.
 RX MEDLINE=94094324; PubMed=7916660;
 RA Pollak M.R., Brown E.M., Chou Y.-H.W., Hebert S.C., Marx S.J.,
 RA Steinmann B., Levy T., Seidman C.B., Seidman J.G.,
 RT "Mutations in the human Ca(2+)-sensing receptor gene cause familial
 RT hypocalcemic hypocalcemia and neonatal severe hyperparathyroidism.",
 RL Cell 75:1297-1303 (1993).
 RN [7]
 RP VARIANTS ADH ALA-127.
 RX MEDLINE=95179179; PubMed=7874174;
 RA Pollak M.R., Brown E.M., Estep H.L., McLaine P.N., Kifor O., Park J.,
 RA Hebert S.C., Seidman C.B., Seidman J.G.,
 RT "Autosomal dominant hypocalcemia caused by a Ca(2+)-sensing receptor
 RT gene mutation.",
 RL Nat. Genet. 8:303-307 (1994).
 RN [8]
 RP VARIANTS FHH MET-62, CYS-66, MET-138, GLU-143 AND GLN-227.
 RX MEDLINE=95243222; PubMed=7726161;
 RA Chou Y.-H.W., Pollak M.R., Brand M.L., T888 G., Argyrakis H.,
 RA Atkinson A.B., Papapoulos S.E., Marx S., Brown E.M., Seidman J.G.,
 RA Seidman C.B.,
 RT "Mutations in the human Ca(2+)-sensing-receptor gene that cause
 RT familial hypocalcemic hypocalcemia.",
 RL Am. J. Hum. Genet. 56:1075-1079 (1995).
 RN [9]
 RP SEQUENCE OF 1-61 FROM N.A., AND VARIANT FHH ALA-39.
 RX MEDLINE=95403641; PubMed=7673400; DOI=10.1210/jc.80.9.2594;
 RA Alda K., Kolsh S., Inoue M., Nakazato M., Tawata M., Onaya T.,
 RT "Familial hypocalcemic hypocalcemia associated with mutation in the

RT human Ca(2+)-sensing receptor gene.";
 RL J. Clin. Endocrinol. Metab. 80:2594-2598 (1995).
 RN [10]
 RP VARIANTS NSHPT LEU-227 AND TR-582.
 RX MEDLINE=96222293; PubMed=6675635;
 RA Pearce S.H.S., Trump D., Wooding C., Besser G.M., Chew S.L.,
 RA Grant D.B., Heath D.A., Hughes I.A., Paterson C.R., Whyte M.P.,
 RA Thakker R.V.;
 RT "Calcium-sensing receptor mutations in familial benign hypercalcemia
 and neonatal hyperparathyroidism.";
 RL J. Clin. Invest. 96:2683-2692 (1995).
 RN [11]
 RP VARIANTS FTH THR-116; HIS-681 AND SER-806, AND VARIANT SER-851.
 RX MEDLINE=96311554; PubMed=873126; DOI=10.1093/hmg/5.5.601;
 RA Baron J., Winer K.K., Yanovski J.A., Cunningham A.W., Lane L.,
 RA Zimmerman D., Cutler G.B. Jr.;
 RT "Mutations in the Ca(2+)-sensing receptor gene cause autosomal
 dominant and sporadic hyperparathyroidism.";
 RL Hum. Mol. Genet. 5:601-606 (1996).
 RN [12]
 RP VARIANTS FTH ARG-174.
 RX MEDLINE=97442275; PubMed=929882;
 RA DOI=10.1002/(SICI)1098-1004(1997)10:3<233::AID-HUM9>3.3.CO;2-G;
 RA Ward B.K., Stuckey B.G.A., Gutteridge D.H., Laine N.G., Pullan P.T.,
 RA Ratajczak T.;
 RT "A novel mutation (L174R) in the Ca2+-sensing receptor gene associated
 with familial hypocalcemic hypercalcemia.";
 RL Hum. Mutat. 10:233-235 (1997).
 RN [13]
 RP VARIANT FTH VAL-616.
 RX MEDLINE=99415602; PubMed=10487661; DOI=10.1210/jc.84.9.3036;
 RA Stock J.L., Brown R.S., Baron J., Codre J.A., Mancilla B.,
 RA De Luca F., Ray K., Mericq M.V., Codre J.A., Mancilla B.,
 RA "Autosomal dominant hypoparathyroidism associated with short stature
 and premature osteoarthritis.";
 RL J. Clin. Endocrinol. Metab. 84:3036-3040 (1999).
 RN [14]
 RP VARIANT FTH GHU-557.
 RX MEDLINE=21603857; PubMed=11762699; DOI=10.1385/ENDO.15.3.277;
 RA Nakayama T., Minato W., Nakagawa M., Soma M., Tobe H., Aoi N.,
 RA Koeike K., Sato M., Ozawa Y., Kamatsuse K., Kokubun S.;
 RT "A novel mutation in Ca2+-sensing receptor gene in familial
 hypocalcemic hypercalcemia.";
 RL Endocrine 15:277-282 (2001).
 CC -1- FUNCTION: Senses changes in the extracellular concentration of
 calcium ions. The activity of this receptor is mediated by a G-
 protein that activates a phosphatidylinositol-calcium second
 messenger system.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P41180-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P41180-2; Sequence=VSP_002035;
 CC -1- TISSUE SPECIFICITY: Found in kidney, but not in brain, lung,
 liver, heart, skeletal muscle, or placenta.
 CC -1- DISEASE: Defects in CASR are the cause of familial hypocalcemic
 hypercalcemia, type 1 (FHH) [MIM:145980], in which the receptor
 has reduced activity. FHH is characterized by altered calcium
 homeostasis. Affected individuals exhibit mild or modest
 hypercalcemia, relative hypocalcemia, and inappropriately normal
 PTH levels.
 CC -1- DISEASE: Defects in CASR are the cause of neonatal severe primary
 hyperparathyroidism (NSHPT) [MIM:239200], in which the receptor
 has reduced activity. NSHPT is a rare autosomal recessive life-
 threatening disorder characterized by very high serum calcium
 concentrations, skeletal demineralization, and parathyroid
 hyperplasia. In some instances NSHPT has been demonstrated to be
 the homozygous form of FHH.
 CC -1- DISEASE: Defects in CASR are the cause of autosomal dominant
 hypocalcemia (ADH) [MIM:601198], in which the receptor is
 activated at subnormal Ca(2+) levels.

CC -1- DISEASE: Defects in CASR are the cause of autosomal dominant
 CC hyperparathyroidism (FHH) [MIM:146200]. FHH is characterized by
 CC hypercalcemia and hypophosphatemia due to inadequate secretion of
 CC parathyroid hormone. Symptoms are seizures, tetany and cramps.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC modified and this statement is not removed. Usage by and for commercial
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 CC -----
 CC EMBL, X81086; CAA56990.1; -
 CC EMBL, U20759; AAB6503.1; -
 CC EMBL, U20760; AAB6504.1; -
 CC EMBL, D50855; AAB09453.1; -
 CC EMBL, S83176; AAB64873.1; -
 CC EMBL, S79217; AAB35262.2; -
 CC EMBL, S68032; AAB29413.2; ALT SEQ.
 CC EMBL, S68033; AAB29414.1; -
 CC EMBL, S68036; AAB29415.1; -
 CC EMBL, S81755; AAD14370.1; -
 CC HSP, P23385; IEMK.
 CC Genew, HGNC:1514; CASR.
 CC MIM, 601199; -
 CC MIM, 145980; -
 CC MIM, 239200; -
 CC MIM, 601198; -
 CC MIM, 146200; -
 CC GO, GO:0005887; C: integral to plasma membrane; TAS.
 CC GO, GO:0004930; F: G-protein coupled receptor activity; TAS.
 CC GO, GO:0004435; F: phosphoinositide phospholipase C activity; TAS.
 CC GO, GO:0006874; P: calcium ion homeostasis; TAS.
 CC GO, GO:0005513; P: calcium ion sensing; TAS.
 CC GO, GO:0007635; P: chemosensory behavior; TAS.
 CC GO, GO:0007186; P: G-protein coupled receptor protein signal; TAS.
 CC GO, GO:0009653; P: morphogenesis; TAS.
 CC GO, GO:0001503; P: ossification; TAS.
 CC InterPro, IPR001828; ANF receptor.
 CC InterPro, IPR000068; G_Protein_Receptor.
 CC InterPro, IPR000337; GPCR_Mgr.
 CC Pfam, PF00003; Tm_3; 1.
 CC Pfam, PF01094; ANF receptor; 1.
 CC PRINTS, PR00248; GPCRMR.
 CC PROSITE, PS00979; G_PROTEIN_RECP_F3_1; 1.
 CC PROSITE, PS00980; G_PROTEIN_RECP_F3_2; 1.
 CC PROSITE, PS00981; G_PROTEIN_RECP_F3_3; 1.
 CC -----
 CC Query Match 74.8%; Score 4044.5; DB 1; Length 1078;
 CC Best Local Similarity 74.0%; Pred. No. 2,86-274;
 CC Matches 782; Conservative 86; Mismatches 138; Indels 51; Gaps 7;
 CC -----
 CC QY 1 MAOLHCOLLFTGLTSLVSVSGYGNQRAOKGDIILGLFPIHFGVAANDOLKSRPE 60
 CC DB 1 MAFVSCCVMLALT-----WHTSAYGPORAKDKDIIIGLFIHFGVAADOLKSRPE 56
 CC QY 61 ATKICIRYNGFRLQMTAIBEINNSMTPLPITLGYVIFPDCTVSRALETLSFVA 120
 CC DB 57 SVBCIRYNFGFRLQMTAIBEINNSPALPLPLTGYVIFPDCTVSRALETLSFVA 116
 CC QY 121 QNKIDSLNLFPCNCSDHPISTIAVVGATSGISTAVANLGLFYIPQVYASSRLLSN 180
 CC DB 117 QNKIDSLNLFPCNCSDHPISTIAVVGATSGISTAVANLGLFYIPQVYASSRLLSN 176
 CC QY 181 KMEKATLRTIPDDEQATMAIIEHFQNNVGTAAADDYRPGIDKREBAVKRDIC 240
 CC DB 177 KNQFKSPLRTIPDDEQATMAIIEHFQNNVGTAAADDYRPGIDKREBAVKRDIC 236
 CC QY 241 IDSEMSOYVTKOLEFIADVONSAKYIVFSGPDLEPILOIYVRNITDRITLAS 300
 CC DB 237 IDSELSOYSDREBIOHVEVIONSTAKYIVFSGPDLEPILOIYVRNITDRITLAS 296

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QY 301 EAMASSSLIAKBYFHYVGTGTFPALBGRIFGFKFLKEVHPSRSDNGFVKEFWETEF 360
DB 297 EAMASSSLIAMQYFHYVGTGTFPALBGRIFGFKFLKEVHPSRSDNGFVKEFWETEF 356
QY 361 NCYFPEKTLTOLKNSKVPBHGPAQDGSKAGNSRRTALRHCCTGEBNITSVETPYDYT 420
DB 357 NCHLOBGAKPL---PVDTFLAGHESGDRFNS--STARPLCTGDENISSVETPYDYT 412
QY 421 HLRISVYVAVYSIAHALODIHSCKEPTGIRANGSCADIKKYVEMOVLNHLIKFTNS 480
DB 413 HLRISVYVAVYSIAHALODIHSCKEPTGIRANGSCADIKKYVEMOVLNHLIKFTNS 472
QY 481 MGEQVDFPDQGLKNGYTIYINMOLSAEDRSYLFHEKYNAYAKSPGDRINNEKLIMG 540
DB 473 MGEQVDFPDQGLKNGYTIYINMOLSAEDRSYLFHEKYNAYAKSPGDRINNEKLIMG 532
QY 541 PSKVVPFNSCNDVCGTRKGIIEGPTCCFECMACABGFSDENDASACTCPDPMFN 600
DB 533 PSKVVPFNSCNDVCGTRKGIIEGPTCCFECMACABGFSDENDASACTCPDPMFN 592
QY 601 ENHTSCIANKIERYLWTEPFGIALTPAVGLIITSFVLGVFKENTPIVAKTNELSY 660
DB 593 ENHTSCIANKIERYLWTEPFGIALTPAVGLIITSFVLGVFKENTPIVAKTNELSY 652
QY 661 LLIPLSLICR8SSSLIFGEPRDWTCLROPAFISFVLICSLIVKTNRLVFEAKIPT 720
DB 653 LLIPLSLICR8SSSLIFGEPRDWTCLROPAFISFVLICSLIVKTNRLVFEAKIPT 712
QY 721 SLRHKWGLMQLFLVPLCLIVLTCIIMLYTAPSPSYNHLIIDEVIFITCDEGLMA 780
DB 713 SLRHKWGLMQLFLVPLCLIVLTCIIMLYTAPSPSYNHLIIDEVIFITCDEGLMA 772
QY 781 LGFLIGYTCLLAALCFPPAFKSRLLPENFNKAITTSMILFVWISFIPAVYSTYKX 840
DB 773 LGFLIGYTCLLAALCFPPAFKSRLLPENFNKAITTSMILFVWISFIPAVYSTYKX 832
QY 841 VSAVEVTAIIAASSGGLGCTIYFNKCYIILFKPCNTIIEVYACSTAAHAFKVAATLRS 900
DB 833 VSAVEVTAIIAASSGGLGCTIYFNKCYIILFKPCNTIIEVYACSTAAHAFKVAATLRS 892
QY 901 AASRKRSSSLCGSTISSPASSTCGPG-----LTMEM 931
DB 893 NVSKRSSSLCGSTISSPASSTCGPG-----LTMEM 952
QY 932 Q-----RCSTQVSPFGSGTFLSLSEFETGRYATLSTRKNSADGRGDDLPSSHH 984
DB 953 QORRQQRCK-OKVTFSGTFTLSFDEPOKNAMHRNSTHONSLEAKSSDTLTH- 1010
QY 985 DQGPQKCEPOPANDARYKAAPTKTLSPGSKERP 1021
DB 1011 -----QPLPLPCCGTDLDLTVOETGLQPVGGDQR 1042

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RA Brown & M., Gamba G., Riccardi D., Lombardi M., Butters R., Klor O.,
RA Sun A., Hediger M.A., Lytton J., Hebert S.C.
RT "Cloning and characterization of an extracellular Ca(2+)-sensing
RL receptor from bovine parathyroid."
RL Nature 366:575-580(1993).
CC -1- FUNCTION: Senses changes in the extracellular concentration of
CC calcium ions. The activity of this receptor is mediated by a G-
CC protein that activates a phosphatidylinositol-calcium second
CC messenger system.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.
CC -----
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.1sb-slb.ch/announce/
CC or send an email to license@1sb-slb.ch).
CC -----
DR EMBL: S67307; AA29171.1; -.
DR PIR: S40476; S40476.
DR HSSP: P23385; 1EWT.
DR InterPro: IPR001828; ANF receptor.
DR InterPro: IPR000068; Ca_sens receptor.
DR InterPro: IPR000337; GPCR_Mgr.
DR Pfam: PF00003; 7tm_3; 1.
DR Pfam: PF01094; ANF_receptor; 1.
DR PRINTS: PR00248; GPCRMR.
DR PROSITE: PS00979; G_PROTEIN_RECP_F3_1; 1.
DR PROSITE: PS00980; G_PROTEIN_RECP_F3_2; 1.
DR PROSITE: PS00981; G_PROTEIN_RECP_F3_3; 1.
DR PROSITE: PS0259; G_PROTEIN_RECP_F3_4; 1.
DR G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.
KW SIGNAL 1 19
FT CHAIN 20 1085
FT DOMAIN 20 613
FT TRANSMEM 614 636
FT TRANSMEM 637 650
FT TRANSMEM 651 671
FT TRANSMEM 672 682
FT TRANSMEM 683 701
FT TRANSMEM 702 725
FT TRANSMEM 726 746
FT TRANSMEM 747 770
FT TRANSMEM 771 793
FT TRANSMEM 807 829
FT TRANSMEM 830 837
FT DOMAIN 838 863
FT TRANSMEM 864 1085
FT DOMAIN 91 91
FT CARBOHYD 131 131
FT CARBOHYD 262 262
FT CARBOHYD 288 288
FT CARBOHYD 401 401
FT CARBOHYD 447 447
FT CARBOHYD 469 469
FT CARBOHYD 489 489
FT CARBOHYD 542 542
FT CARBOHYD 595 595
SQ SEQUENCE 1085 AA; 121170 MW; 5D66DB8C9CD13E47 CRC64;
Query Match 73.94; Score 3999.5; DB 1; Length 1085;
Best Local Similarity 72.84; Pred. No. 4e-271;
Matches 778; Conservative 92; Mismatches 141; Indels 57; Gaps 8;
QY 1 MAQLHQLLFTGTLTOSYVSGYGNQRAQKDDIILGSLPIHFGVAARDQDKSRPE 60
DB 1 MALVSCCHILAFS---TWTSATGPDPRAKKDDIILGSLPIHFGVAARDQDKSRPE 57
QY 61 ATKIRYVGRGFRWLQAMTFAIBEINSMFTLPNTTGYRIFDTCNTYSKALENTLSFVA 120

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Db      58 SVEICIRYNGFRMTQAMIFAIIEINSSPALLPMTLGRIDTCNTVSKALEATLSFVA 117
Qy      121 ONKIDSLNDEFCONSDHI PSTIAYVATGSGISTAVANLGLFYIPOVYASSSRLSN 180
Db      118 ONKIDSLNDEFCONSDHI PSTIAYVATGSGISTAVANLGLFYIPOVYASSSRLSN 177
Qy      181 KNEYKAFLEPTPNDEQOATAMABITIEHOMVWGLTADDDYGRPGIDKPREBAVKDIDC 240
Db      178 KNEYKAFLEPTPNDEQOATAMABITIEHOMVWGLTADDDYGRPGIDKPREBAVKDIDC 237
Qy      241 IDSEMILOYTQKLEFIADIVIONSNAKIVVSNBDEPLLOEYRENTDIRIMLAS 300
Db      238 IDSEMILOYTQKLEFIADIVIONSNAKIVVSNBDEPLLOEYRENTDIRIMLAS 297
Qy      301 EAAASSLLAKPEYFHVVGTTIGFALPAGRI PGFNKLEKEVPSRSDNGFVPEMETP 360
Db      298 EAAASSLLAKPEYFHVVGTTIGFALPAGRI PGFNKLEKEVPSRSDNGFVPEMETP 357
Qy      361 NCYFEKTLTQLKNSKVPVSHGPAAGDGSANANSRRTALHPCTGBENITSVETPYDIT 420
Db      358 NCYFEKTLTQLKNSKVPVSHGPAAGDGSANANSRRTALHPCTGBENITSVETPYDIT 413
Qy      421 HIRISYNYVAVYSIAHALODIHSCKRGISIPANGSCADIKKYEANQVNLHLIKFTNS 480
Db      414 HIRISYNYVAVYSIAHALODIHSCKRGISIPANGSCADIKKYEANQVNLHLIKFTNS 473
Qy      481 MGEYVDPDQDGLKNTIINNQLSADSVLFHEVGNANAYAKOSDRINEXKILWSG 540
Db      474 MGEYVDPDQDGLKNTIINNQLSADSVLFHEVGNANAYAKOSDRINEXKILWSG 533
Qy      541 FSKVVPFNSCRDVCPTGRKGIIEBPTCCFPCMA CAGSEFSDENDASACTCPDNFMSN 600
Db      534 FSKVVPFNSCRDVCPTGRKGIIEBPTCCFPCMA CAGSEFSDENDASACTCPDNFMSN 593
Qy      601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGIILTSFTLGFPIKRNTPYKATNRELISY 660
Db      594 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGIILTSFTLGFPIKRNTPYKATNRELISY 653
Qy      661 LILFSLICCFSSSILFI GEPDWTCLRLQAPAGISFVLCISCIIVKTNRLVLEAKIPT 720
Db      654 LILFSLICCFSSSILFI GEPDWTCLRLQAPAGISFVLCISCIIVKTNRLVLEAKIPT 713
Qy      721 SLRRKXVNLQPLVLCILVQVTCITIMLYTAPSSSYNHELEDEVIETCDGSLMA 780
Db      714 SLRRKXVNLQPLVLCILVQVTCITIMLYTAPSSSYNHELEDEVIETCDGSLMA 773
Qy      781 LGLIGTCLLAIICFPFAKSKRLPENFEAKPTISMLIFPIVWISFIPAVYSTYGR 840
Db      774 LGLIGTCLLAIICFPFAKSKRLPENFEAKPTISMLIFPIVWISFIPAVYSTYGR 833
Qy      841 VSAVEYIAIILASFGILGCTIYFNKYIILFKPCRNTEIEVRGTAHAAPVATRLRS 900
Db      834 VSAVEYIAIILASFGILGCTIYFNKYIILFKPCRNTEIEVRGTAHAAPVATRLRS 893
Qy      901 AASRKSLLCGSTISSPASSTG-----P 925
Db      894 AASRKSLLCGSTISSPASSTG-----P 925
Qy      926 GUTMEMO-----RSTOKVSGSGTYLTLSTFETGXYATLSTARSNSADGRSGD 978
Db      954 GUTMEMO-----RSTOKVSGSGTYLTLSTFETGXYATLSTARSNSADGRSGD 978
Qy      979 LPSRHHDGPPKCEBOPANDARYKAPTKGTLESFGSKENPTIMEE 1026
Db      1013 LPSRHHDGPPKCEBOPANDARYKAPTKGTLESFGSKENPTIMEE 1012

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RESULT 4
CASR_RAT STANDARD; PRT; 1079 AA.
AC P48442;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)

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DT      25-OCT-2004 (Rel. 45, Last annotation update)
DE      Extracellular calcium-sensing receptor precursor (CASR) (Parathyroid
DE      Cell calcium-sensing receptor)
GN      Name=Casr; Synonyms=Gprc2a, Pcalr;
OS      Rattus norvegicus (Rat);
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Sprague-Dawley; TISSUE=Kidney outer medulla;
RX      MEDLINE=95241465; PubMed=7724534;
RA      Riccardi D., Park J., Lee W., Gamba G., Brown E.M., Hebert S.C.,
RT      "Cloning and functional expression of a rat kidney extracellular
RT      calcium/polyvalent cation-sensing receptor."
RL      Proc. Natl. Acad. Sci. U.S.A. 92:131-135(1995).
RN      [2]
RP      SEQUENCE OF 1-294 FROM N.A.
RC      STRAIN=Wistar;
RX      MEDLINE=95241465; PubMed=7724534;
RA      Ruat M., Snowman A.M., Snyder S.H.;
RT      "Calcium sensing receptor: molecular cloning in rat and localization
RT      to nerve terminals."
RL      Proc. Natl. Acad. Sci. U.S.A. 92:3161-3165(1995).
CC      -1- FUNCTION: Senses changes in the extracellular concentration of
CC      calcium ions. The activity of this receptor is mediated by a G-
CC      protein that activates a phosphatidylinositol-calcium second
CC      messenger system.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC      at the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC      or send an email to license@ebi.ac.uk).
CC      -----
DR      EMBL; U10354; AAC52149.1; -
DR      EMBL; U20289; AAC52195.1; -
DR      PIR; I59362; I59362.
DR      HSP; P23385; IEMX.
DR      RCD; 2277; Casr.
DR      InterPro; IPR001828; ANP_receptor.
DR      InterPro; IPR000068; Ca_sens_receptor.
DR      Pfam; PF00003; 7em_3; 1.
DR      Pfam; PF01094; ANP_receptor; 1.
DR      PRINTS; PR00248; GPCRMR.
DR      PROSITE; PS00979; G_PROTEIN_REC_P3_1; 1.
DR      PROSITE; PS00980; G_PROTEIN_REC_P3_2; 1.
DR      PROSITE; PS00981; G_PROTEIN_REC_P3_3; 1.
DR      PROSITE; PS00982; G_PROTEIN_REC_P3_4; 1.
KW      G-protein coupled receptor; Glycophorin; Signal; Transmembrane.
FT      SIGNAL 1..19
FT      CHAIN 20..1079
FT      DOMAIN 20..612
FT      TRANSSEM 613..635
FT      DOMAIN 636..649
FT      TRANSSEM 650..670
FT      DOMAIN 671..681
FT      TRANSSEM 682..700
FT      DOMAIN 701..724
FT      TRANSSEM 725..745
FT      DOMAIN 746..769
FT      TRANSSEM 770..792
FT      DOMAIN 793..805
FT      TRANSSEM 806..828
FT      DOMAIN 829..836
FT      TRANSSEM 837..862
FT      DOMAIN 863..1079
FT      CARBOHYD 90

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Extracellular calcium-sensing receptor.
1 (Potential).
Cytosolic (Potential).
2 (Potential).
Extracellular (Potential).
3 (Potential).
Cytosolic (Potential).
4 (Potential).
Extracellular (Potential).
5 (Potential).
Cytosolic (Potential).
6 (Potential).
Extracellular (Potential).
7 (Potential).
Cytosolic (Potential).
N-linked (GlcNAc...) (Potential).

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FT CARBOHYD 130 130 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 261 261 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 287 287 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 366 366 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 446 446 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 468 468 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 488 488 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 541 541 N-linked (GlcNAc...) (potential)
 FT CARBOHYD 594 594 N-linked (GlcNAc...) (potential)
 SQ SEQUENCE 1079 AA, 120867 MW, D766450361F9736 CRC64;

Query Match 73.9%; Score 3996; DB 1; Length 1079;
 Best Local Similarity 73.7%; Pred. No. 6,9e-271;
 Matches 780; Conservative 85; Mismatches 140; Indels 54; Gaps 8;

QY 1 MAOLHCOLLFLGFTLLQSYNGVGNQRAQKGDIIILGLFPIHFVAAKODLKSRE 60
 DB 1 MASYSCCLALLAL-----AMHSAYGPDQRAQKGDIIILGLFPIHFVAAKODLKSRE 56
 QY 61 ATKCRNPNPGRPMLOMIFALIEINNSMTPLNITIGRIDTCNTVSKALEATLSFVA 120
 DB 57 SVECIIRNPNRGRPMLOMIFALIEINNSMTPLNITIGRIDTCNTVSKALEATLSFVA 116
 QY 121 QNKIDSLNDEFNCSDHIPSTIAVVGATSGISTAVANLGLFYIPQVYASSRLLSN 180
 DB 117 QNKIDSLNDEFNCSDHIPSTIAVVGATSGISTAVANLGLFYIPQVYASSRLLSN 176
 QY 181 KNEYKAFLERTIPNDEQATMAEIIIEHPQNNVGTLLAADDYGRPGIDKREBEAVKRDIC 240
 DB 177 KNEYKAFLERTIPNDEQATMAEIIIEHPQNNVGTLLAADDYGRPGIDKREBEAERDIC 236
 QY 241 IDFSMISQYTKQKLEFIADYTONSSNAVIVYFNSNGPLLELLOEYRNRITDTITWAS 300
 DB 237 IDFSMISQYTKQKLEFIADYTONSSNAVIVYFNSNGPLLELLOEYRNRITDTITWAS 296
 QY 301 EAMASSSLIAKPEYFHVVGITGIPALRAGRIQPKNFKLEKVPSSSDNGFYKSEWSETF 360
 DB 297 EAMASSSLIAKPEYFHVVGITGIPALRAGRIQPKNFKLEKVPSSSDNGFYKSEWSETF 356
 QY 361 NCYFTEKTLTQK-NSKVPSHGPAAGDGSKAGNSRRALRHPGTGENITSVETPYLDY 419
 DB 357 NCYFTEKTLTQK-NSKVPSHGPAAGDGSKAGNSRRALRHPGTGENITSVETPYLDY 411
 QY 420 THLRISYNNVAVVSIHALODIHSCKPCTGIPANGSCADIKKGAQVLANLILKXTN 479
 DB 412 THLRISYNNVAVVSIHALODIHSCKPCTGIPANGSCADIKKGAQVLANLILKXTN 471
 QY 480 SMGQVDPDQDGLKGNVTIIMQIQAEDSVLPFHVGNVYNAKPSDRILNINEKILMS 539
 DB 472 SMGQVDPDQDGLKGNVTIIMQIQAEDSVLPFHVGNVYNAKPSDRILNINEKILMS 531
 QY 540 GSKVVPFNSGRCDCVPGTRKGIIEGPTCCFECNACAGEPSDENASACTKCPDNFWS 599
 DB 532 GSKVVPFNSGRCDCVPGTRKGIIEGPTCCFECNACAGEPSDENASACTKCPDNFWS 591
 QY 600 NENHTSCIAKEIYLSWTERPGIATITPAVLGILITSPYLGIFITFRNTPYKATNRIS 659
 DB 592 NENHTSCIAKEIYLSWTERPGIATITPAVLGILITSPYLGIFITFRNTPYKATNRIS 651
 QY 660 YLLPSLICCFFSSSLIFIGEPDMTCRLRQAPAGISFVLCISIVKTNRLVLVEAKIP 719
 DB 652 YLLPSLICCFFSSSLIFIGEPDMTCRLRQAPAGISFVLCISIVKTNRLVLVEAKIP 711
 QY 720 TSLHRKVGNLQPLLVLCILVQIVTCIIMLYTAPSSYRNHLEDEVIFITCDGSSLM 779
 DB 712 TSLHRKVGNLQPLLVLCILVQIVTCIIMLYTAPSSYRNHLEDEVIFITCDGSSLM 771
 QY 780 ALGFLIGTCLLAACFPFAFKSRLLPENFNKATITPSMLIFTVMSIFIPAYSTYTGK 839
 DB 772 ALGFLIGTCLLAACFPFAFKSRLLPENFNKATITPSMLIFTVMSIFIPAYSTYTGK 831
 QY 840 FVSAVEVIALIASFGILGCIYFNKCYILFPICNTLIEVASCRAAHAFVAAATLRR 899

DB 832 FVSAVEVIALIASFGILGCIYFNKCYILFPICNTLIEVASCRAAHAFVAAATLRR 891
 QY 900 SAARRKSSSLICGTTSPASSSTGPG-----LTME 930
 DB 892 PNIRKSSSSISGTTSPASSSTGPG-----LTME 951
 QY 931 MQ-----RSTQKSPGSGVTTLSLSEETGRVATLSTARSNSADGRSGDULPSR 982
 DB 952 PQQQQQPQQRCK-QKTIPEGSTVTFSLSDPEQKNAMAHNSWRQNSLEAGNSNDTLGR 1010
 QY 983 HHQGPQKCEPQPDANDARYAAPTKTLESFGSKERP 1021
 DB 1011 H-----QALLPLQCADASEMTIQETLQGPWGDHQP 1043

RESULT 5

ID 0802A8 PRELIMINARY; PRT; 1079 AA.
 AC 0802A8;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Rattus norvegicus (Rat).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCBITaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Miscar; TISSUE=Dorsal root ganglion;
 RA Bukoski R., Bian K., Wang Y.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY244122; A059490.1; -.
 DR HSSP; P23385; IEMK.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like receptor. .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR0001828; ANF_receptor.
 DR InterPro; IPR000068; Ca_sens_receptor.
 DR InterPro; IPR000337; GPCR_Mgt.
 DR Pfam; PF00003; 7tm_3; 1.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR Pfam; PF07562; NCD3G; 1.
 DR PRINTS; PR00592; CASSENSING.
 DR PRINTS; PR00248; GPCRMR.
 DR PROSITE; PS00979; G_PROTEIN_RECPE_F3_1; 1.
 DR PROSITE; PS00980; G_PROTEIN_RECPE_F3_2; 1.
 DR PROSITE; PS00981; G_PROTEIN_RECPE_F3_3; 1.
 DR PROSITE; PS50259; G_PROTEIN_RECPE_F3_4; 1.
 RM Receptor.
 SQ SEQUENCE 1079 AA; 120830 MW; 50A2D026AE65CE81 CRC64;

Query Match 73.7%; Score 3986; DB 2; Length 1079;
 Best Local Similarity 73.5%; Pred. No. 3,5e-270;
 Matches 778; Conservative 87; Mismatches 140; Indels 54; Gaps 8;

QY 1 MAOLHCOLLFLGFTLLQSYNGVGNQRAQKGDIIILGLFPIHFVAAKODLKSRE 60
 DB 1 MASYSCCLALLAL-----AMHSAYGPDQRAQKGDIIILGLFPIHFVAAKODLKSRE 56
 QY 61 ATKCRNPNPGRPMLOMIFALIEINNSMTPLNITIGRIDTCNTVSKALEATLSFVA 120
 DB 57 SVECIIRNPNRGRPMLOMIFALIEINNSMTPLNITIGRIDTCNTVSKALEATLSFVA 116
 QY 121 QNKIDSLNDEFNCSDHIPSTIAVVGATSGISTAVANLGLFYIPQVYASSRLLSN 180
 DB 117 QNKIDSLNDEFNCSDHIPSTIAVVGATSGISTAVANLGLFYIPQVYASSRLLSN 176
 QY 181 KNEYKAFLERTIPNDEQATMAEIIIEHPQNNVGTLLAADDYGRPGIDKREBEAVKRDIC 240
 DB 177 KNEYKAFLERTIPNDEQATMAEIIIEHPQNNVGTLLAADDYGRPGIDKREBEAERDIC 236